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3  
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BATCH  
2-12-01RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/688,286DATE: 02/14/2001  
TIME: 10:31:01Input Set : A:\688286.txt  
Output Set: N:\CRF3\02142001\I688286.raw

4 <110> APPLICANT: Willson, Tracy  
5 Nicola, Nicos A.  
6 Hilton, Douglas J.  
7 Metcalf, Donald  
8 Zhang, Jian G.  
10 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES  
11 ENCODING SAME  
13 <130> FILE REFERENCE: Davies cc  
15 <140> CURRENT APPLICATION NUMBER: US/09/688,286  
16 <141> CURRENT FILING DATE: 2000-10-13  
18 <150> PRIOR APPLICATION NUMBER: 09/051,843  
19 <151> PRIOR FILING DATE: 1998-06-29  
21 <160> NUMBER OF SEQ ID NOS: 8  
23 <170> SOFTWARE: PatentIn Ver. 2.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 1383  
27 <212> TYPE: DNA  
28 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4  
30 <220> FEATURE:  
31 <221> NAME/KEY: CDS  
32 <222> LOCATION: (61)..(1338)  
34 <220> FEATURE:  
35 <221> NAME/KEY: unsure  
36 <222> LOCATION: (121)  
37 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this  
38 region  
40 <220> FEATURE:  
41 <221> NAME/KEY: unsure  
42 <222> LOCATION: (122)  
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48 <222> LOCATION: (123)  
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50 region  
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54 <222> LOCATION: (640)  
55 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this  
56 region  
58 <220> FEATURE:  
59 <221> NAME/KEY: unsure  
60 <222> LOCATION: (641)  
61 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this  
62 region  
64 <220> FEATURE:

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65 <221> NAME/KEY: unsure
66 <222> LOCATION: (642)
67 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
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74 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg 108
75 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Val Leu Leu Leu Trp
76 1 5 10 15
W--> 78 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca 156
W--> 79 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
80 20 25 30
82 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
83 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
84 35 40 45
86 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
87 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
88 50 55 60
90 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
91 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
92 65 70 75 80
94 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
95 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
96 85 90 95
98 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg 396
99 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
100 100 105 110
102 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg 444
103 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
104 115 120 125
106 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
107 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
108 130 135 140
110 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac 540
111 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
112 145 150 155 160
114 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat 588
115 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
116 165 170 175
118 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa 636
119 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
120 180 185 190
W--> 122 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat 684
W--> 123 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
124 195 200 205
126 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat 732
127 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
128 210 215 220
130 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt 780

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131 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
132 225                      230                      235                      240
134 gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc    828
135 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
136                      245                      250                      255
138 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat    876
139 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
140                      260                      265                      270
142 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga    924
143 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
144                      275                      280                      285
146 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac    972
147 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
148                      290                      295                      300
150 gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt    1020
151 Ala Val Tyr Thr Val Arg Val Lys Thr Asn Lys Leu Cys Phe
152 305                      310                      315                      320
154 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt    1068
155 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
156                      325                      330                      335
158 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca    1116
159 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
160                      340                      345                      350
162 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg    1164
163 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
164                      355                      360                      365
166 ctt aag atc att ata ttt cct cca att cct gat cct gcc aag att ttt    1212
167 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
168                      370                      375                      380
170 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag    1260
171 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
172 385                      390                      395                      400
174 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg    1308
175 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
176                      405                      410                      415
178 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc    1358
179 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
180                      420                      425
182 tttcttgccct tcaatgtgac cctgt                      1383
186 <210> SEQ ID NO: 2
187 <211> LENGTH: 426
188 <212> TYPE: PRT
189 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4
191 <220> FEATURE:
192 <221> NAME/KEY: unsure
193 <222> LOCATION: (21)
194 <223> OTHER INFORMATION: authors are unsure about the sequence assignment
196 <220> FEATURE:
197 <221> NAME/KEY: unsure

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198 <222> LOCATION: (194)  
 199 <223> OTHER INFORMATION: authors are unsure about the sequence assignment  
 201 <400> SEQUENCE: 2

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 203 1 5 10 15  
 W--> 205 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro  
 206 20 25 30  
 208 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile  
 209 35 40 45  
 211 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg  
 212 50 55 60  
 214 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu  
 215 65 70 75 80  
 217 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln  
 218 85 90 95  
 220 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu  
 221 100 105 110  
 223 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val  
 224 115 120 125  
 226 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser  
 227 130 135 140  
 229 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr  
 230 145 150 155 160  
 232 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr  
 233 165 170 175  
 235 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu  
 236 180 185 190  
 W--> 238 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn  
 239 195 200 205  
 241 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr  
 242 210 215 220  
 244 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly  
 245 225 230 235 240  
 247 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys  
 248 245 250 255  
 250 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn  
 251 260 265 270  
 253 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg  
 254 275 280 285  
 256 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp  
 257 290 295 300  
 259 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe  
 260 305 310 315 320  
 262 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly  
 263 325 330 335  
 265 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro  
 266 340 345 350  
 268 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg  
 269 355 360 365

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271 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
272   370           375           380
274 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
275 385           390           395           400
277 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
278   405           410           415
280 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
281   420           425
284 <210> SEQ ID NO: 3
285 <211> LENGTH: 1383
286 <212> TYPE: DNA
287 <213> ORGANISM: IL-13 receptor alpha-chain
289 <220> FEATURE:
290 <221> NAME/KEY: CDS
291 <222> LOCATION: (61)..(1338)
293 <400> SEQUENCE: 3
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297 atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc 108
298 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
299   1           5           10           15
301 gcc ggc ggc ggg ggc ggg ggc ggg gcg cct acg gaa act cag cca 156
302 Ala Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
303   20           25           30
305 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
306 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
307   35           40           45
309 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
310 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
311   50           55           60
313 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300
314 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
315 65           70           75           80
317 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348
318 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
319   85           90           95
321 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
322 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
323 100           105           110
325 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg 444
326 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
327 115           120           125
329 act gaa ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct 492
330 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
331 130           135           140
333 tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac 540
334 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
335 145           150           155           160
337 tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt 588
338 Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/688,286

DATE: 02/14/2001  
TIME: 10:31:02

Input Set : A:\688286.txt  
Output Set: N:\CRF3\02142001\I688286.raw

L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
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L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2